Nucleic Acid Sciences

Author Index to Volume 44

Allen, M. D. See Tateno, M., 335
Amano, N. See Tateno, M., 335
Arnold, E. See Ding, J., 125

Benight, A. S. See Owczarzy, R., 217
Benight, A. S. See Schurr, J. M., 283
Berger, I.
—; Cai, L.; Chen, L.; Rich, A.: Energetics of the Lattice: Packing Elements in Crystals of Four-Stranded Intercalated Cytosine-Rich DNA Molecules, 257
Berman, H. M. Crystal Studies of B-DNA: The Answers and the Questions, 23
Bloomfield, V. A. DNA Condensation by Multivalent Cations, 269
Breslauer, K. J. Editorial to Volume 44, No. 2, 1997, 123
Breslauer, K. J. See Goodman, M., 1
Brown, T.
—; Hunter, W. N.: Non-Watson–Crick Base Associations in DNA and RNA Revealed by Single Crystal X-Ray Diffraction Methods: Mismatches, Modified Bases, and Nonduplex DNA, 91

Cai, L. See Berger, I., 257
Carey, J. See Szwajkajzer, D., 181
Chaires, J. B. Editorial to Volume 44, No. 3, 1997, 199
Chaires, J. B. Energetics of Drug–DNA Interactions, 201
Cheng, X. See Lloyd, R. S., 139
Chen, L. See Berger, I., 257
Chiu, T. K. See Dickerson, R. E., 361

Delrow, J. J. See Schurr, J. M., 283
Dickerson, R. E. Editorial to Volume 44, No. 4, 1997, 321
Dickerson, R. E.
—; Chiu, T. K.: Helix Bending as a Factor in Protein/DNA Recognition, 361
Ding, J.
—; Hughes, S. H.; Arnold, E.: Protein–Nucleic Acid Interactions and DNA Conformation in a Complex of Human Immunodeficiency Virus Type 1 Reverse Transcriptase with a Double-Stranded DNA Template-Primer, 125
Drew, H. See Travers, A., 423

Fujimoto, B. S. See Schurr, J. M., 283

Gallo, F. J. See Owczarzy, R., 217
Goodman, M.
—; Breslauer, K. J.: Editorials to Vol. 44, Issue 1, 1997, 1
Goodsell, D. S. See Walker, W. L., 323

Holbrook, S. R.
—; Kim, S.-H.: RNA Crystallography, 3
Ho, P. S.
—; Mooers, B. H. M.: Z-DNA Crystallography, 65
Hughes, S. H. See Ding, J., 125
Hunter, W. N. See Brown, T., 91

Jen-Jacobson, L. Protein–DNA Recognition Complexes: Conservation of Structure and Binding Energy in the Transition State, 153

Kakinuma, J. See Tateno, M., 335
Kim, S.-H. See Holbrook, S. R., 3
Koike, H. See Tateno, M., 335
Kopka, M. L. See Walker, W. L., 323

Lane, M. J. See Owczarzy, R., 217
Lloyd, R. S.
—; Cheng, X.: Mechanistic Link Between DNA Methyltransferases and DNA Repair Enzymes by Base Flipping, 139

Mooers, B. H. M. See Ho, P. S., 65

Neidle, S. Crystallographic Insights into DNA Minor Groove Recognition by Drugs, 105

Owczarzy, R.
—; Vallone, P. M.; Gallo, F. J.; Paner, T. M.; Lane, M. J.; Benight, A. S.: Predicting Sequence-Dependent Melting Stability of Short Duplex DNA Oligomers, 217

Paner, T. M. See Owczarzy, R., 217

Plum, G. E. Thermodynamics of Oligonucleotide Triple Helices, 241

Rich, A. See Berger, I., 257

SantaLucia, J., Jr.
—; Turner, D. H.: Measuring the Thermodynamics of RNA Secondary Structure Formation, 309

Schurr, J. M.
—; Delrow, J. J.; Fujimoto, B. S.; Benight, A. S.: The Question of Long-Range Allosteric Transitions in DNA, 283

Suck, D. DNA Recognition by Structure-Selective Nucleases, 405

Sundaralingam, M. See Wahl, M. C., 45

Suzuki, M. See Tateno, M., 335

Szwajkajzer, D.
—; Carey, J.: Molecular and Biological Constraints on Ligand-Binding Affinity and Specificity, 181

Tateno, M.
—; Yamasaki, K.; Amano, N.; Kakinuma, J.; Koike, H.; Allen, M. D.; Suzuki, M.: DNA Recognition by ;gb-Sheets, 335

Travers, A.
—; Drew, H.: DNA Recognition and Nucleosome Organization, 423

Turner, D. H. See SantaLucia, J., Jr., 309

Vallone, P. M. See Owczarzy, R., 217

Wahl, M. C.
—; Sundaralingam, M.: Crystal Structures of A-DNA Duplexes, 45

Walker, W. L.
—; Kopka, M. L.; Goodsell, D. S.: Progress in the Design of DNA Sequence-Specific Lexitropsins, 323

Yamasaki, K. See Tateno, M., 335

Nucleic Acid Sciences

Subject Index to Volume 44

Adaptability, 181
Adaptation, 153
Additivity, 181
A-DNA bending, 45
A-DNA crystal structure, 45
A-form DNA, 45
AIDS, 125
Antigene, 241
Antisense, 241

Base flipping, 139
Base mispairing, 45
B-DNA, 23, 361
Binding energy, 153

Calorimetry, 201
Catalytic RNA, 3
Conformation, 65
Conformational fluctuations, 423
Conformational range, 23
Crystal engineering, 257
Crystal lattice and packing, 257
Crystal packing, 45
Crystal packing motif, 23
Crystal structure, 3
Crystal structures, 105
Crystallography, 23
Curvature, 361

Deformation, 423
Dinucleotide parameter, 335
Disproportionation, 241
DNA, 91, 201, 323
DNA-binding protein, 423
DNA condensation, 269
DNA crystallography, 257
DNA kinetics, 269
DNA methyltransferases, 139
DNA morphology, 269
DNA–protein interaction, 335
DNA recognition, 335, 405, 423
DNA repair enzymes, 139
DNA reversibility, 269
DNase I, 405
DNA structure, 125
DNA transcriptional activation, 283
Domain size, 283
Drugs, 201

Enzyme catalysis, 153
Extrahelical nucleotide, 139

Free energy, 201
FREEHELIX, 361

Genomic sequences, 65
Groove binders, 201
G-tetrad, 91

Helix bending, 361
Histone octamer, 423
Hoogsteen, 241
Host–guest chemistry, 181
Hydration, 65
Hydrogen bonds, 91

I-motif, 257
Intercalation, 257
Intercalators, 201
Intermolecular interactions, 181, 257
Internal loop, 3

Kink, 361

Lexitropsins, 323
Long-range allosteric transitions, 283
Loop, 91

Major groove, 335
Measurement errors, 309
Metal ion coordination, 45
Minor groove, 323, 335
Minor groove drugs, 105
Mismatches, 91
Mispairs, 91
Modified bases, 91
Multivalent cations, 269
Mutagenesis, 91

Nonspecific binding, 153
Non-Watson–Crick base pairs, 91
5′-nucleases, 405
Nucleic acid hydration, 45
Nucleic acids, 257
Nucleosome recognition, 423
Nucleotide, 65

Oligomers, 217
Oligonucleotides, 105
Optical melting, 309

P1 and S1 nucleases, 405
Phase diagram, 241

Polyelectrolyte effect, 201
Polymerase structure, 125
Polymers, 65
Preorganization, 181
Protein-DNA complexes, 423
Protein–DNA interaction, 125
Protein–DNA recognition, 153, 361

Quadruplexes, 91

Rational drug design, 181, 323
Review, 3
Ribozyme, 3
RNA, 3, 91, 309
Roll, 361

Secondary structure, 283, 309
Sequence recognition, 105
Sequence-dependent hybridization reactions, 217
Sequence-dependent melting stability, 217
Sequence-specific binding, 153
Sequence-specific polyamides, 323
β-sheet, 335
Short duplex DNA, 217
Single crystals, 65
Solvent-accessible surface area, 201
Spermine binding, 45
State diagram, 241
Statistical mechanics, 269
Structure-selective nucleases, 405

T4 endonuclease VII, 405
Thermodynamics, 153, 201, 309
Tilt, 361
Torsoids, 269
Transfer RNA, 3
Transition state, 153
Triplex, 241
Triplexes, 91

Watson–Crick base pairs, 91
Writhe, 361

X-ray crystallography, 3
X-ray crystallography, 125
X-ray structure, 405

Z-DNA, 65